

10/511796

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SEQUENCE LISTING

<110> SODE, Koji

<120> Glucose dehydrogenase beta-subunit and DNA encoding the same

<130> TOYA126.002APC

<141> 2003-04-25

<150> JP 2002-125353

<151> 2002-04-26

<160> 19

<170> PatentIn Ver. 2.0

<210> 1

<211> 2467

<212> DNA

<213> Burkholderia cepacia

<220>

<221> CDS

<222> (258)..(761)

<220>

<221> CDS

<222> (764)..(2380)

<220>

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<222> (2386)..(2466)

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tacgaatggc tgacacatttgc aatggactat aaaaccatttgc tccgttccgg aatgtgcgcg 180
tacatttcag gtccgcgcgcg atttttgaga aatatcaagc gtggttttcc cgaatccgg 240
gttcgagaga aggaaac atg cac aac gac aac act ccc cac tcg cgt cgc 290

Met His Asn Asp Asn Thr Pro His Ser Arg Arg

1 5 10

cac ggc gac gca gcc gca tca ggc atc acg cgg cgt caa tgg ttg caa 338
His Gly Asp Ala Ala Ala Ser Gly Ile Thr Arg Arg Gln Trp Leu Gln
15 20 25

ggc gcg ctg gcg ctg acc gca gcg ggc ctc acg ggt tcg ctg aca ttg 386
Gly Ala Leu Ala Leu Thr Ala Ala Gly Leu Thr Gly Ser Leu Thr Leu
30 35 40

cgg gcg ctt gca gac aac ccc ggc act gcg ccg ctc gat acg ttc atg 434
Arg Ala Leu Ala Asp Asn Pro Gly Thr Ala Pro Leu Asp Thr Phe Met
45 50 55

acg ctt tcc gaa tcg ctg acc ggc aag aaa ggg ctc acg cgc gtg atc 482
Thr Leu Ser Glu Ser Leu Thr Gly Lys Lys Gly Leu Ser Arg Val Ile
60 65 70 75

ggc gag cgc ctg ctg cag gcg ctg cag aag ggc tcg ttc aag acg gcc 530
Gly Glu Arg Leu Leu Gln Ala Leu Gln Lys Gly Ser Phe Lys Thr Ala

80	85	90	
gac agc ctg ccg cag ctc gcc ggc gcg ctc gcg tcc ggt tcg ctg acg			578
Asp Ser Leu Pro Gln Leu Ala Gly Ala Leu Ala Ser Gly Ser Leu Thr			
95	100	105	
cct gaa cag gaa tcg ctc gca ctg acg atc ctc gag gcc tgg tat ctc			626
Pro Glu Gln Glu Ser Leu Ala Leu Thr Ile Leu Glu Ala Trp Tyr Leu			
110	115	120	
ggc atc gtc gac aac gtc gtg att acg tac gag gaa gca tta atg ttc			674
Gly Ile Val Asp Asn Val Val Ile Thr Tyr Glu Ala Leu Met Phe			
125	130	135	
ggc gtc gtg tcc gat acg ctc gtg atc cgt tcg tat tgc ccc aac aaa			722
Gly Val Val Ser Asp Thr Leu Val Ile Arg Ser Tyr Cys Pro Asn Lys			
140	145	150	155
ccc ggc ttc tgg gcc gac aaa ccg atc gag agg caa gcc tg atg gcc			769
Pro Gly Phe Trp Ala Asp Lys Pro Ile Glu Arg Gln Ala Met Ala			
160	165	170	
gat acc gat acg caa aag gcc gac gtc gtc gtt gga tcg ggt gtc			817
Asp Thr Asp Thr Gln Lys Ala Asp Val Val Val Val Gly Ser Gly Val			
175	180	185	
gcg ggc gcg atc gtc gcg cat cag ctc gcg atg gcg ggc aag gcg gtg			865
Ala Gly Ala Ile Val Ala His Gln Leu Ala Met Ala Gly Lys Ala Val			
190	195	200	
atc ctg ctc gaa gcg ggc ccg cgc atg ccg cgc tgg gaa atc gtc gag			913
Ile Leu Leu Glu Ala Gly Pro Arg Met Pro Arg Trp Glu Ile Val Glu			
205	210	215	
cgc ttc cgc aat cag ccc gac aag atg gac ttc atg gcg ccg tac ccg			961
Arg Phe Arg Asn Gln Pro Asp Lys Met Asp Phe Met Ala Pro Tyr Pro			
220	225	230	
tcg agc ccc tgg gcg ccg cat ccc gag tac ggc ccg ccg aac gac tac			1009
Ser Ser Pro Trp Ala Pro His Pro Glu Tyr Gly Pro Pro Asn Asp Tyr			
235	240	245	250
ctg atc ctg aag ggc gag cac aag ttc aac tcg cag tac atc cgc gcg			1057
Leu Ile Leu Lys Gly Glu His Lys Phe Asn Ser Gln Tyr Ile Arg Ala			
255	260	265	
gtg ggc ggc acg acg tgg cac tgg gcc gcg tcg gcg tgg cgc ttc att			1105
Val Gly Gly Thr Thr Trp His Trp Ala Ala Ser Ala Trp Arg Phe Ile			
270	275	280	
ccg aac gac ttc aag atg aag acg gtg tac ggc gtc ggc cgc gac tgg			1153
Pro Asn Asp Phe Lys Met Lys Ser Val Tyr Gly Val Gly Arg Asp Trp			
285	290	295	
ccg atc cag tac gac gat ctc gag ccg tac tat cag cgc gcg gag gaa			1201
Pro Ile Gln Tyr Asp Asp Leu Glu Pro Tyr Tyr Gln Arg Ala Glu Glu			
300	305	310	
gag ctc ggc gtg tgg ggc ccg ggc ccc gag gaa gat ctg tac tcg ccg			1249
Glu Leu Gly Val Trp Gly Pro Gly Pro Glu Glu Asp Leu Tyr Ser Pro			
315	320	325	330
cgc aag cag ccg tat ccg atg ccg ccg ctg ccg ttg tcg ttc aac gag			1297
Arg Lys Gln Pro Tyr Pro Met Pro Pro Leu Pro Leu Ser Phe Asn Glu			
335	340	345	
cag acc atc aag acg gcg ctg aac aac tac gat ccg aag ttc cat gtc			1345
Gln Thr Ile Lys Thr Ala Leu Asn Asn Tyr Asp Pro Lys Phe His Val			
350	355	360	
gtg acc gag ccg gtc gcg cgc aac agc cgc ccg tac gac ggc cgc ccg			1393
Val Thr Glu Pro Val Ala Arg Asn Ser Arg Pro Tyr Asp Gly Arg Pro			
365	370	375	
act tgt tgc ggc aac aac aac tgc atg ccg atc tgc ccg atc ggc gcg			1441
Thr Cys Cys Gly Asn Asn Asn Cys Met Pro Ile Cys Pro Ile Gly Ala			

380	385	390	
atg tac aac ggc atc gtg cac gtc gag aag gcc gaa cgc gcc ggc gcg Met Tyr Asn Gly Ile Val His Val Glu Lys Ala Glu Arg Ala Gly Ala			1489
395	400	405	410
aag ctg atc gag aac gcg gtc gtc tac aag ctc gag acg ggc ccg gac Lys Leu Ile Glu Asn Ala Val Val Tyr Lys Leu Glu Thr Gly Pro Asp			1537
415	420	425	
aag cgc atc gtc gcg gcg ctc tac aag gac aag acg ggc gcc gag cat Lys Arg Ile Val Ala Ala Leu Tyr Lys Asp Lys Thr Gly Ala Glu His			1585
430	435	440	
cgc gtc gaa ggc aag tat ttc gtg ctc gtc aac ggc atc gag acg Arg Val Glu Gly Lys Tyr Phe Val Leu Ala Ala Asn Gly Ile Glu Thr			1633
445	450	455	
ccg aag atc ctg ctg atg tcc gcg aac cgc gat ttc ccg aac ggt gtc Pro Lys Ile Leu Leu Met Ser Ala Asn Arg Asp Phe Pro Asn Gly Val			1681
460	465	470	
gcg aac agc tcg gac atg gtc ggc cgc aac ctg atg gac cat ccg ggc Ala Asn Ser Ser Asp Met Val Gly Arg Asn Leu Met Asp His Pro Gly			1729
475	480	485	490
acc ggc gtg tcg ttc tat gcg agc gag aag ctg tgg ccg ggc cgc ggc Thr Gly Val Ser Phe Tyr Ala Ser Glu Lys Leu Trp Pro Gly Arg Gly			1777
495	500	505	
ccg cag gag atg acg tcg ctg atc ggt ttc cgc gac ggt ccg ttc cgc Pro Gln Glu Met Thr Ser Leu Ile Gly Phe Arg Asp Gly Pro Phe Arg			1825
510	515	520	
gcg acc gaa gcg gcg aag aag atc cac ctg tcg aac ctg tcg cgc atc Ala Thr Glu Ala Ala Lys Lys Ile His Leu Ser Asn Leu Ser Arg Ile			1873
525	530	535	
gac cag gag acg cag aag atc ttc aag gcc ggc aag ctg atg aag ccc Asp Gln Glu Thr Gln Lys Ile Phe Lys Ala Gly Lys Leu Met Lys Pro			1921
540	545	550	
gac gag ctc gac gcg cag atc cgc gac cgt tcc gca cgc tac gtg cag Asp Glu Leu Asp Ala Gln Ile Arg Asp Arg Ser Ala Arg Tyr Val Gln			1969
555	560	565	570
ttc gac tgc ttc cac gaa atc ctg ccg caa ccc gag aac cgc atc gtg Phe Asp Cys Phe His Glu Ile Leu Pro Gln Pro Glu Asn Arg Ile Val			2017
575	580	585	
ccg agc aag acg gcg acc gat gcg atc ggc att ccg cgc ccc gag atc Pro Ser Lys Thr Ala Thr Asp Ala Ile Gly Ile Pro Arg Pro Glu Ile			2065
590	595	600	
acg tat gcg atc gac gac tac gtg aag cgc ggc gcc gcg cat acg cgc Thr Tyr Ala Ile Asp Asp Tyr Val Lys Arg Gly Ala Ala His Thr Arg			2113
605	610	615	
gag gtc tac gcg acc gcc gcg aag gtg ctc ggc ggc acg gac gtc gtg Glu Val Tyr Ala Thr Ala Ala Lys Val Leu Gly Gly Thr Asp Val Val			2161
620	625	630	
ttc aac gac gaa ttc gcg ccg aac aat cac atc acg ggc tcg acg atc Phe Asn Asp Glu Phe Ala Pro Asn Asn His Ile Thr Gly Ser Thr Ile			2209
635	640	645	650
atg ggc gcc gat gcg cgc gac tcc gtc gtc gac aag gac tgc cgc acg Met Gly Ala Asp Ala Arg Asp Ser Val Val Asp Lys Asp Cys Arg Thr			2257
655	660	665	
ttc gac cat ccg aac ctg ttc att tcg agc agc ggc acg atg ccg acc Phe Asp His Pro Asn Leu Phe Ile Ser Ser Ala Thr Met Pro Thr			2305
670	675	680	
gtc ggt acc gta aac gtg acg ctg acg atc gcc gcg ctc gcg ctg cgg Val Gly Thr Val Asn Val Thr Leu Thr Ile Ala Ala Leu Ala Leu Arg			2353

685	690	695
atg tcg gac acg ctg aag aag gaa gtc tgacc gtg cgg aaa tct act ctc		2403
Met Ser Asp Thr Leu Lys Lys Glu Val	Val Arg Lys Ser Thr Leu	
700	705	710
act ttc ctc atc gcc ggc tgc ctc gcg ttg ccg ggc ttc gcg cgc gcg		2451
Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu Pro Gly Phe Ala Arg Ala		
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Ala Asp Ala Ala Asp		
730		

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<212> PRT
<213> Burkholderia cepacia

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Thr Ala Ala Gly Leu Thr Gly Ser Leu Thr Leu Arg Ala Leu Ala Asp			
35	40	45	
Asn Pro Gly Thr Ala Pro Leu Asp Thr Phe Met Thr Leu Ser Glu Ser			
50	55	60	
Leu Thr Gly Lys Lys Gly Leu Ser Arg Val Ile Gly Glu Arg Leu Leu			
65	70	75	80
Gln Ala Leu Gln Lys Gly Ser Phe Lys Thr Ala Asp Ser Leu Pro Gln			
85	90	95	
Leu Ala Gly Ala Leu Ala Ser Gly Ser Leu Thr Pro Glu Gln Glu Ser			
100	105	110	
Leu Ala Leu Thr Ile Leu Glu Ala Trp Tyr Leu Gly Ile Val Asp Asn			
115	120	125	
Val Val Ile Thr Tyr Glu Glu Ala Leu Met Phe Gly Val Val Ser Asp			
130	135	140	
Thr Leu Val Ile Arg Ser Tyr Cys Pro Asn Lys Pro Gly Phe Trp Ala			
145	150	155	160
Asp Lys Pro Ile Glu Arg Gln Ala			
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<210> 3
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<212> PRT
<213> Burkholderia cepacia

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20	25	30	
Ala Val Ile Leu Leu Glu Ala Gly Pro Arg Met Pro Arg Trp Glu Ile			
35	40	45	
Val Glu Arg Phe Arg Asn Gln Pro Asp Lys Met Asp Phe Met Ala Pro			
50	55	60	
Tyr Pro Ser Ser Pro Trp Ala Pro His Pro Glu Tyr Gly Pro Pro Asn			
65	70	75	80
Asp Tyr Leu Ile Leu Lys Gly Glu His Lys Pro Phe Asn Ser Gln Tyr Ile			

85	90	95
Arg Ala Val Gly	Gly Thr Thr Trp His	Trp Ala Ala Ser Ala Trp Arg
100	105	110
Phe Ile Pro Asn Asp Phe Lys	Met Lys Ser Val Tyr Gly	Val Gly Arg
115	120	125
Asp Trp Pro Ile Gln Tyr	Asp Asp Leu Glu Pro	Tyr Tyr Gln Arg Ala
130	135	140
Glu Glu Leu Gly Val	Trp Gly Pro Gly	Pro Glu Glu Asp Leu Tyr
145	150	155
Ser Pro Arg Lys Gln Pro	Tyr Pro Met Pro	Pro Leu Pro Leu Ser Phe
165	170	175
Asn Glu Gln Thr Ile Lys	Thr Ala Leu Asn Asn	Tyr Asp Pro Lys Phe
180	185	190
His Val Val Thr Glu Pro	Val Ala Arg Asn Ser Arg	Pro Tyr Asp Gly
195	200	205
Arg Pro Thr Cys Cys Gly	Asn Asn Asn Cys Met	Pro Ile Cys Pro Ile
210	215	220
Gly Ala Met Tyr Asn Gly	Ile Val His Val	Glu Lys Ala Glu Arg Ala
225	230	235
Gly Ala Lys Leu Ile Glu	Asn Ala Val Val	Tyr Lys Leu Glu Thr Gly
245	250	255
Pro Asp Lys Arg Ile Val	Ala Ala Leu Tyr Lys Asp Lys	Thr Gly Ala
260	265	270
Glu His Arg Val Glu Gly	Lys Tyr Phe Val Leu Ala	Ala Asn Gly Ile
275	280	285
Glu Thr Pro Lys Ile Leu	Leu Met Ser Ala Asn Arg	Asp Phe Pro Asn
290	295	300
Gly Val Ala Asn Ser Ser	Asp Met Val Gly Arg	Asn Leu Met Asp His
305	310	315
Pro Gly Thr Gly Val	Ser Phe Tyr Ala	Ser Glu Lys Leu Trp Pro Gly
325	330	335
Arg Gly Pro Gln Glu Met	Thr Ser Leu Ile Gly	Phe Arg Asp Gly Pro
340	345	350
Phe Arg Ala Thr Glu Ala	Ala Lys Ile His	Leu Ser Asn Leu Ser
355	360	365
Arg Ile Asp Gln Glu Thr	Gln Lys Ile Phe Lys	Ala Gly Lys Leu Met
370	375	380
Lys Pro Asp Glu Leu Asp	Ala Gln Ile Arg	Asp Arg Ser Ala Arg Tyr
385	390	395
Val Gln Phe Asp Cys	Phe His Glu Ile Leu	Pro Gln Pro Glu Asn Arg
405	410	415
Ile Val Pro Ser Lys	Thr Ala Thr Asp Ala	Ile Gly Ile Pro Arg Pro
420	425	430
Glu Ile Thr Tyr Ala Ile	Asp Asp Tyr Val Lys	Arg Gly Ala Ala His
435	440	445
Thr Arg Glu Val Tyr	Ala Thr Ala Ala Lys	Val Leu Gly Gly Thr Asp
450	455	460
Val Val Phe Asn Asp	Glu Phe Ala Pro	Asn Asn His Ile Thr Gly Ser
465	470	475
Thr Ile Met Gly Ala	Asp Ala Arg Asp	Ser Val Val Asp Lys Asp Cys
485	490	495
Arg Thr Phe Asp His	Pro Asn Leu Phe	Ile Ser Ser Ser Ala Thr Met
500	505	510
Pro Thr Val Gly Thr Val	Asn Val Thr Leu Thr	Ile Ala Ala Leu Ala
515	520	525
Leu Arg Met Ser Asp Thr	Leu Lys Lys Glu Val	
530	535	

<210> 4
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<212> PRT
<213> Burkholderia cepacia

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Val Arg Lys Ser Thr Leu Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu
1 5 10 15
Pro Gly Phe Ala Arg Ala Ala Asp Ala Ala Asp
20 25

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<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 5
cccaagcttg ggccgataacc gatacgca 28

<210> 6
<211> 29
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: primer

<400> 6
gagaagcttt ccgcacggtc agacttcc 29

<210> 7
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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catgccatgg cacacaacga caacact 27

<210> 8
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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cccaagcttg ggtcagactt ccttcttcag c 31

<210> 9

<211> 16
<212> PRT
<213> Burkholderia cepacia

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Ala Asp Ala Ala Asp Pro Ala Leu Val Lys Arg Gly Glu Tyr Leu Ala
1 5 10 15

<210> 10
<211> 25
<212> PRT
<213> Artificial Sequence

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<222> (6,17,18,19,22)
<223> Xaa=unknown

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Ala Asp Ala Ala Asp Xaa Ala Leu Val Lys Arg Gly Glu Tyr Leu Ala
1 5 10 15
Xaa Xaa Xaa Asp Cys Xaa Ala Cys His
20 25

□!<210> 11
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<212> DNA
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<222> (673)..(1950)

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cggccgcag gatatgacgt cgctgatcggt ttccgcac ggccgttcc gcgcgaccga 120
agccgcgaag aagatccatc tgcgaacat gtccgcata aaccaggaga cgcagaagat 180
cttcaaggcc ggcaaactga tgaagcacga ggagctcgac ggcgcagatcc ggcaccgttc 240
cgcgctac gtgcagttcg actgcttcca cgagattctg cccgcagcccc agaaccgcata 300
cgtgccgagc aagacggcca ccgacgcgtat cggatcccg cgcgcgaga tcacgtatgc 360
gatcgacgt tacgtgaagc gcggcgccgt gcacacgcgc gaggtctacg cgacggccgc 420
gaaggtgctg ggcggcaccg acgtcgctt caacgcacgat ttcgcgcga acaaccacat 480
cacggcgcg aggatcatgg ggcgcgatgc acgcgcactcg gtcgtcgaca aggactgccc 540
cacttcgac catccgaacc tggcgttctc gagcagctcg acgatgccga ccgtcggtac 600
ggtaacgtg acgctgacga tcgcggcgat cgcgcgtcg atgtcgacca cgctgaagaa 660
ggaagtctga cc gtg cgg aaa tct act ctc acc ttc ctc ctc gcc ggc tgc 711
Val Arg Lys Ser Thr Leu Thr Phe Leu Leu Ala Gly Cys

1 5 10
ctc gcg ctg ccc ggc ctc gca cgc gcg gcc gat tcg gcc gat ccg gcg 759
Leu Ala Leu Pro Gly Leu Ala Arg Ala Ala Asp Ser Ala Asp Pro Ala
15 20 25

cat gtc aag cgc ggc gaa tac ctc gcc gtc gcg ggc gac tgc atg gca 807
His Val Lys Arg Gly Glu Tyr Leu Ala Val Ala Gly Asp Cys Met Ala
30 35 40 45

tgc cac acc gcg aag ggc ggc aag ccg ttc gcg ggc ctc ggc atg		855	
Cys His Thr Ala Lys Gly Gly Lys Pro Phe Ala Gly Gly Leu Gly Met			
50	55	60	
ccg gtg ccg atg ctc ggc aag atc tat acg agc aac atc aca ccg gat		903	
Pro Val Pro Met Leu Gly Lys Ile Tyr Thr Ser Asn Ile Thr Pro Asp			
65	70	75	
ccc gat acc ggc atc ggc aac tgg acg ttc gag gac ttc gag cgc gcg		951	
Pro Asp Thr Gly Ile Gly Asn Trp Thr Phe Glu Asp Phe Glu Arg Ala			
80	85	90	
gtg cgg cac ggc gta tcg aag aac ggc gac aac ctg tac ccg gcg atg		999	
Val Arg His Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met			
95	100	105	
ccg tac gtg tcg tac gcg aag atc aac gac gac gtg caa gcg ctg		1047	
Pro Tyr Val Ser Tyr Ala Lys Ile Asn Asp Asp Asp Val Gln Ala Leu			
110	115	120	125
tac gcg tac ttc atg cac ggc gtc gaa ccg gtc aag cag gcg ccg ccg		1095	
Tyr Ala Tyr Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro			
130	135	140	
aag aac gag atc ccc gcg ctg ctg agc atg cgc tgg ccg ctg aag atc		1143	
Lys Asn Glu Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile			
145	150	155	
tgg aac tgg ctg ttc ctg aag gac ggc gtg tac cag ccg aag ccc gag		1191	
Trp Asn Trp Leu Phe Leu Lys Asp Gly Val Tyr Gln Pro Lys Pro Glu			
160	165	170	
cag agc gcc gag tgg aac cgc ggc gcc tat ctc gtg cag ggc ctc gcg		1239	
Gln Ser Ala Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala			
175	180	185	
cac tgc agc acg tgc cac acg ccg cgc ggc atc gcg atg cag gag aag		1287	
His Cys Ser Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys			
190	195	200	205
tcg ctc gac gaa acg ggc agc ttc ctg tcg ggc tcg gtg ctc gcg		1335	
Ser Leu Asp Glu Thr Gly Ser Phe Leu Ser Gly Ser Val Leu Ala			
210	215	220	
ggc tgg gac ggc tac aac atc acg tcc gac ccg aac gcg ggg atc ggc		1383	
Gly Trp Asp Gly Tyr Asn Ile Thr Ser Asp Pro Asn Ala Gly Ile Gly			
225	230	235	
ggc tgg acg cag cag cag ctc gtc cag tac ctg cgc acc ggc agc gtg		1431	
Gly Trp Thr Gln Gln Leu Val Gln Tyr Leu Arg Thr Gly Ser Val			
240	245	250	
ccg ggc ctc gcg cag gcg gcc ggc ccg atg gcc gag gcg atc gag cac		1479	
Pro Gly Leu Ala Gln Ala Ala Gly Pro Met Ala Glu Ala Ile Glu His			
255	260	265	
agc ttc tcg aag atg acc gaa gcc gac atc ggc ggc ccg atg gcc gag		1527	
Ser Phe Ser Lys Met Thr Glu Ala Asp Ile Gly Gly Pro Met Ala Glu			
270	275	280	285
gcg atc gag cac agc ttc tcg aag atg acc gaa gcc gac atc ggc cgc		1575	
Ala Ile Glu His Ser Phe Ser Lys Met Thr Glu Ala Asp Ile Gly Arg			
290	295	300	
tcg tcg tgg ggc aag ccg gcc gag gat ggc ctg aag ctg cgc ggc gtc		1623	
Ser Ser Trp Gly Lys Pro Ala Glu Asp Gly Leu Lys Leu Arg Gly Val			
305	310	315	
gcg ctc gcg tcg tcg ggc atc gat ccg gca ccg ctg tat ctc ggc aac		1671	
Ala Leu Ala Ser Ser Gly Ile Asp Pro Ala Pro Leu Tyr Leu Gly Asn			
320	325	330	
tgc gcg acc tgc cac cag atg cag ggc aag ggc acg ccg gac ggt tac		1719	
Cys Ala Thr Cys His Gln Met Gln Gly Lys Gly Thr Pro Asp Gly Tyr			
335	340	345	

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Tyr Pro Pro Leu Phe His Asn Ser Thr Val Gly Ala Ser Asn Pro Thr	
350 355 360 365	
aac ctc gtg cag gtg atc ctg aac ggc gtg cag cgc aag gcc ggc agc	1815
Asn Leu Val Gln Val Ile Leu Asn Gly Val Gln Arg Lys Ala Gly Ser	
370 375 380	
gag gac gtc ggg atg ccc gcg ttc cgc cac gag ctg tcg gat gcg cag	1863
Glu Asp Val Gly Met Pro Ala Phe Arg His Glu Leu Ser Asp Ala Gln	
385 390 395	
atc gcc gcg ctg acg aac tac ctg acg ggg cag ttc ggc aat ccg gcc	1911
Ile Ala Ala Leu Thr Asn Tyr Leu Thr Gly Gln Phe Gly Asn Pro Ala	
400 405 410	
gcg aag gtg acc gag cag gac gtc gcg aag ctg cgc tga aacgcggcac	1960
Ala Lys Val Thr Glu Gln Asp Val Ala Lys Leu Arg	
415 420 425	
gcggcgaggc agggcaaca tagaaaagag gaggagcaca gcacatcgaa cggggccccga	2020
tgcgggtgt tgcagagcgg gacgggcggc gcaggcggtc gcccgtcctg gttcacaggc	2080
aatccggcgc ggcacgcgg cgcatcggtt tcggtgatcg agaccatgac accgaaccaa	2140
ccgttctcg cgtcccgacgc cgatgtgctg ctgctgctgt cccgaatcct gctcggtatc	2200
ctgttcgtga tgttcggtcg gaagaagatt atcgacttct cccgtacgat cgcggtatcg	2260
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<400> 12
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20 25 30
Arg Gly Glu Tyr Leu Ala Val Ala Gly Asp Cys Met Ala Cys His Thr
35 40 45
Ala Lys Gly Gly Lys Pro Phe Ala Gly Leu Gly Met Pro Val Pro
50 55 60
Met Leu Gly Lys Ile Tyr Thr Ser Asn Ile Thr Pro Asp Pro Asp Thr
65 70 75 80
Gly Ile Gly Asn Trp Thr Phe Glu Asp Phe Glu Arg Ala Val Arg His
85 90 95
Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met Pro Tyr Val
100 105 110
Ser Tyr Ala Lys Ile Asn Asp Asp Asp Val Gln Ala Leu Tyr Ala Tyr
115 120 125
Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro Lys Asn Glu
130 135 140
Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile Trp Asn Trp
145 150 155 160
Leu Phe Leu Lys Asp Gly Val Tyr Gln Pro Lys Pro Glu Gln Ser Ala
165 170 175
Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala His Cys Ser
180 185 190
Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys Ser Leu Asp
195 200 205
Glu Thr Gly Gly Ser Phe Leu Ser Gly Ser Val Leu Ala Gly Trp Asp

210	215	220	
Gly	Tyr Asn Ile Thr Ser Asp Pro Asn Ala Gly	Ile Gly Gly Trp Thr	
225	230	235	240
Gln Gln Gln Leu Val Gln Tyr Leu Arg Thr Gly Ser Val Pro Gly Leu			
245	250	255	
Ala Gln Ala Ala Gly Pro Met Ala Glu Ala Ile Glu His Ser Phe Ser			
260	265	270	
Lys Met Thr Glu Ala Asp Ile Gly Gly Pro Met Ala Glu Ala Ile Glu			
275	280	285	
His Ser Phe Ser Lys Met Thr Glu Ala Asp Ile Gly Arg Ser Ser Trp			
290	295	300	
Gly Lys Pro Ala Glu Asp Gly Leu Lys Leu Arg Gly Val Ala Leu Ala			
305	310	315	320
Ser Ser Gly Ile Asp Pro Ala Pro Leu Tyr Leu Gly Asn Cys Ala Thr			
325	330	335	
Cys His Gln Met Gln Gly Lys Gly Thr Pro Asp Gly Tyr Tyr Pro Pro			
340	345	350	
Leu Phe His Asn Ser Thr Val Gly Ala Ser Asn Pro Thr Asn Leu Val			
355	360	365	
Gln Val Ile Leu Asn Gly Val Gln Arg Lys Ala Gly Ser Glu Asp Val			
370	375	380	
Gly Met Pro Ala Phe Arg His Glu Leu Ser Asp Ala Gln Ile Ala Ala			
385	390	395	400
Leu Thr Asn Tyr Leu Thr Gly Gln Phe Gly Asn Pro Ala Ala Lys Val			
405	410	415	
Thr Glu Gln Asp Val Ala Lys Leu Arg			
420	425		

<210> 13
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 13
tgcaccgtgc ggaaatctac tctcact

27

<210> 14
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 14
acttccttct tcagcgtgtc cgacatc

27

□;<210> 15
<211> 1441
<212> DNA
<213> Burkholderia cepacia

<220>
<221> CDS

<222> (121)..(1398)

<400> 15
tccgaacctg ttcatttcga gcagcgcgac gatgccgacc gtcggtaccc taaacgtgac 60
gctgacgatc gcccgcctcg cgctgcggat gtcggacacg ctgaagaagg aagtctgacc 120
gtg cgg aaa tct act ctc act ttc ctc atc gcc ggc tgc ctc gcg ttg 168
Val Arg Lys Ser Thr Leu Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu
1 5 10 15
ccg ggc ttc gcg cgc ggc gat ggc gat ccg ggc ctg gtc aag 216
Pro Gly Phe Ala Arg Ala Ala Asp Ala Ala Asp Pro Ala Leu Val Lys
20 25 30
cgc ggc gaa tac ctc gcg acc gcc atg ccg atg ctc ggc aag 264
Arg Gly Glu Tyr Leu Ala Thr Ala Met Pro Val Pro Met Leu Gly Lys
35 40 45
atc tac acg agc aac atc acg ccc gat ccc gat acg ggc gac tgc atg 312
Ile Tyr Thr Ser Asn Ile Thr Pro Asp Pro Asp Thr Gly Asp Cys Met
50 55 60
gcc tgc cac acc gtg aag ggc ggc aag ccg tac gcg ggc ggc ctt ggc 360
Ala Cys His Thr Val Lys Gly Gly Lys Pro Tyr Ala Gly Gly Leu Gly
65 70 75 80
ggc atc ggc aaa tgg acg ttc gag gac ttc gag ccg gcg gtc cgg cac 408
Gly Ile Gly Lys Trp Thr Phe Glu Asp Phe Glu Arg Ala Val Arg His
85 90 95
ggc gtg tcg aag aac ggc gac aac ctg tat ccg gcg atg ccg tac gtg 456
Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met Pro Tyr Val
100 105 110
tcg tac gcg aag atc aag gac gac gac gta cgc gcg ctg tac gcc tac 504
Ser Tyr Ala Lys Ile Lys Asp Asp Asp Val Arg Ala Leu Tyr Ala Tyr
115 120 125
ttc atg cac ggc gtc gag ccg gtc aag cag gcg ccg ccg aag aac gag 552
Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro Lys Asn Glu
130 135 140
atc cca gcg ctg cta agc atg cgc tgg ccg ctg aag atc tgg aac tgg 600
Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile Trp Asn Trp
145 150 155 160
ctg ttc ctg aag gac ggc ccg tac cag ccg aag ccg tcg cag agc gcc 648
Leu Phe Leu Lys Asp Gly Pro Tyr Gln Pro Lys Pro Ser Gln Ser Ala
165 170 175
gaa tgg aat cgc ggc gcg tat ctg gtg cag ggt ctc gcg cac tgc agc 696
Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala His Cys Ser
180 185 190
acg tgc cac acg ccg cgc ggc atc gcg atg cag gag aag tcg ctc gac 744
Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys Ser Leu Asp
195 200 205
gaa acc ggc ggc agc ttc ctc gcg ggg tcg gtc ctc gcc ggc tgg gac 792
Glu Thr Gly Gly Ser Phe Leu Ala Gly Ser Val Leu Ala Gly Trp Asp
210 215 220
ggc tac aac atc acg tcg gac ccg aat gcg ggg atc ggc agc tgg acg 840
Gly Tyr Asn Ile Thr Ser Asp Pro Asn Ala Gly Ile Gly Ser Trp Thr
225 230 235 240
cag cag cag ctc gtg cag tat ttg cgc acc ggc agc gtg ccg ggc gtc 888
Gln Gln Gln Leu Val Gln Tyr Leu Arg Thr Gly Ser Val Pro Gly Val
245 250 255
gcg cag gcg gcc ggg ccg atg gcc gag ggc gtc gag cac agc ttc tcg 936
Ala Gln Ala Ala Gly Pro Met Ala Glu Ala Val Glu His Ser Phe Ser
260 265 270
aag atg acc gaa gcg gac atc ggt gcg atc gcc acg tac gtc cgc acg 984

Lys Met Thr Glu Ala Asp Ile Gly Ala Ile Ala Thr Tyr Val Arg Thr			
275	280	285	
gtg ccg gcc gtt gcc gac agc aac gcg aag cag ccc cggt tcg tgg			1032
Val Pro Ala Val Ala Asp Ser Asn Ala Lys Gln Pro Arg Ser Ser Trp			
290	295	300	
ggc aag ccg gcc gag gac ggg ctg aag ctg cgc ggt gtc gcg ctc gcg			1080
Gly Lys Pro Ala Glu Asp Gly Leu Lys Leu Arg Gly Val Ala Leu Ala			
305	310	315	320
tcg tcg ggc atc gat ccg gcg ctg tat ctc ggc aac tgc gcg acg			1128
Ser Ser Gly Ile Asp Pro Ala Arg Leu Tyr Leu Gly Asn Cys Ala Thr			
325	330	335	
tgc cac cag atg cag ggc aag ggc acg ccg gac ggc tat tac ccg tcg			1176
Cys His Gln Met Gln Gly Lys Gly Thr Pro Asp Gly Tyr Tyr Pro Ser			
340	345	350	
ctg ttc cac aac tcc acc gtc ggc gcg tcg aat ccg tcg aac ctc gtg			1224
Leu Phe His Asn Ser Thr Val Gly Ala Ser Asn Pro Ser Asn Leu Val			
355	360	365	
cag gtg atc ctg aac ggc gtg cag cgc aag atc ggc agc gag gat atc			1272
Gln Val Ile Leu Asn Gly Val Gln Arg Lys Ile Gly Ser Glu Asp Ile			
370	375	380	
ggg atg ccc gct ttc cgc tac gat ctg aac gac gcg cag atc gcc gcg			1320
Gly Met Pro Ala Phe Arg Tyr Asp Leu Asn Asp Ala Gln Ile Ala Ala			
385	390	395	400
ctg acg aac tac gtg acc gcg cag ttc ggc aat ccg gcg gcg aag gtg			1368
Leu Thr Asn Tyr Val Thr Ala Gln Phe Gly Asn Pro Ala Ala Lys Val			
405	410	415	
acg gag cag gac gtc gcg aag ctg cgc tga catagtcggg cgcgccgaca			1418
Thr Glu Gln Asp Val Ala Lys Leu Arg			
420	425		
cggcgcaacc gataggacag gag			1441

<210> 16

<211> 425

<212> PRT

<213> Burkholderia cepacia

<400> 16

Val Arg Lys Ser Thr Leu Thr Phe Leu Ile Ala Gly Cys Leu Ala Leu			
1	5	10	15
Pro Gly Phe Ala Arg Ala Ala Asp Ala Ala Asp Pro Ala Leu Val Lys			
20	25	30	
Arg Gly Glu Tyr Leu Ala Thr Ala Met Pro Val Pro Met Leu Gly Lys			
35	40	45	
Ile Tyr Thr Ser Asn Ile Thr Pro Asp Pro Asp Thr Gly Asp Cys Met			
50	55	60	
Ala Cys His Thr Val Lys Gly Gly Lys Pro Tyr Ala Gly Gly Leu Gly			
65	70	75	80
Gly Ile Gly Lys Trp Thr Phe Glu Asp Phe Glu Arg Ala Val Arg His			
85	90	95	
Gly Val Ser Lys Asn Gly Asp Asn Leu Tyr Pro Ala Met Pro Tyr Val			
100	105	110	
Ser Tyr Ala Lys Ile Lys Asp Asp Asp Val Arg Ala Leu Tyr Ala Tyr			
115	120	125	
Phe Met His Gly Val Glu Pro Val Lys Gln Ala Pro Pro Lys Asn Glu			
130	135	140	
Ile Pro Ala Leu Leu Ser Met Arg Trp Pro Leu Lys Ile Trp Asn Trp			
145	150	155	160

Leu Phe Leu Lys Asp Gly Pro Tyr Gln Pro Lys Pro Ser Gln Ser Ala
165 170 175
Glu Trp Asn Arg Gly Ala Tyr Leu Val Gln Gly Leu Ala His Cys Ser
180 185 190
Thr Cys His Thr Pro Arg Gly Ile Ala Met Gln Glu Lys Ser Leu Asp
195 200 205
Glu Thr Gly Gly Ser Phe Leu Ala Gly Ser Val Leu Ala Gly Trp Asp
210 215 220
Gly Tyr Asn Ile Thr Ser Asp Pro Asn Ala Gly Ile Gly Ser Trp Thr
225 230 235 240
Gln Gln Gln Leu Val Gln Tyr Leu Arg Thr Gly Ser Val Pro Gly Val
245 250 255
Ala Gln Ala Ala Gly Pro Met Ala Glu Ala Val Glu His Ser Phe Ser
260 265 270
Lys Met Thr Glu Ala Asp Ile Gly Ala Ile Ala Thr Tyr Val Arg Thr
275 280 285
Val Pro Ala Val Ala Asp Ser Asn Ala Lys Gln Pro Arg Ser Ser Trp
290 295 300
Gly Lys Pro Ala Glu Asp Gly Leu Lys Leu Arg Gly Val Ala Leu Ala
305 310 315 320
Ser Ser Gly Ile Asp Pro Ala Arg Leu Tyr Leu Gly Asn Cys Ala Thr
325 330 335
Cys His Gln Met Gln Gly Lys Gly Thr Pro Asp Gly Tyr Tyr Pro Ser
340 345 350
Leu Phe His Asn Ser Thr Val Gly Ala Ser Asn Pro Ser Asn Leu Val
355 360 365
Gln Val Ile Leu Asn Gly Val Gln Arg Lys Ile Gly Ser Glu Asp Ile
370 375 380
Gly Met Pro Ala Phe Arg Tyr Asp Leu Asn Asp Ala Gln Ile Ala Ala
385 390 395 400
Leu Thr Asn Tyr Val Thr Ala Gln Phe Gly Asn Pro Ala Ala Lys Val
405 410 415
Thr Glu Gln Asp Val Ala Lys Leu Arg
420 425

<210> 17
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: heme binding motif

<220>
<221> UNSURE
<222> (2,3)
<223> Xaa=unknown

<400> 17
Cys Xaa Xaa Cys His
1 5

<210> 18
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 18
catgccatgg cacacaacga caacact

27

<210> 19
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 19
cccaagcttg ggtcagactt ccttcttcag c

31